SEQUENCE LISTING

SEQ ID NO 1

```
acattctaac tgcaaccttt cgaagccttt gctctggcac aacaggtagt aggcgacact 60
gttcgtgttg tcaacatgac caacaagtgt ctcctccaaa ttgctctcct gttgtgcttc 120
tccactacag ctctttccat gagctacaac ttgcttggat tcctacaaag aagcagcaat 180
tttcagtgtc agaagctcct gtggcaattg aatgggaggc ttgaatactg cctcaaggac 240
aggatgaact ttgacatccc tgaggagatt aagcagctgc agcagttcca gaaggaggac 300
gccgcattga ccatctatga gatgctccag aacatctttg ctattttcag acaagattca 360
tctagcactg gctggaatga gactattgtt gagaacctcc tggctaatgt ctatcatcag 420
ataaaccatc tgaagacagt cctggaagaa aaactggaga aagaagattt caccagggga 480
aaactcatga gcagtctgca cctgaaaaga tattatggga ggattctgca ttacctgaag 540
gccaaggagt acagtcactg tgcctggacc atagtcagag tggaaatcct aaggaacttt 600
tacttcatta acagacttac aggttacctc cgaaactgaa gatctcctag cctgtgcctc 660
tgggactgga caattgcttc aagcattctt caaccagcag atgctgttta agtgactgat 720
ggctaatgta ctgcatatga aaggacacta gaagattttg aaatttttat taaattatga 780
gttattttta tttatttaaa ttttattttg gaaaataaat tatttttggt gcaaaagtca 840
```

SEQ ID NO 2 (Propeptide constitutes amino acid residues 1-21)

```
Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser
  1               5                  10                  15

Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
             20                  25                  30

Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
          35                  40                  45

Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
      50                  55                  60

Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
 65                  70                  75                  80

Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
                 85                  90                  95

Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
            100                 105                 110

Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
        115                 120                 125

Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
    130                 135                 140

Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
145                 150                 155                 160

His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
                165                 170                 175

Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
            180                 185
```

SEQ ID NO 3

cgtttaaacttaagcttcgccacc**atg**accaacaagtgcctgctccagatcgccctgctcctgtgcttcagcaccacggccctatcgatgagctac
aacctgctcggcttcctgcagaggagttcgaacttccagtgccagaagctcctgtggcagctgaacgggcgcctggagtactgcctgaaggaca
ggatgaacttcgacatccccgaggaaatcaagcagctgcagcagttccagaaggaggacgccgctctgaccatctacgagatgctgcagaac
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cgcatcctgcactacctgaaggccaaggagtacagccactgcgcctggaccatcgtacgcgtggagatcctgcgcaacttctacttcatcaacc
gcctgaccggctacctgcgcaactgataaggatccactagtccagtgtggtg

The bolded atg is the first codon of the propeptide, the underlined atg the first codon of the mature interferon β sequence.